



Fig. 1

COesterase: domain 1 of 1, from 44 to 545: score 552.8, E = 2.3e-162

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vldAtkypPsClQdddfgfsldLKvalkmlslgwnklvgklslsEDCLYL
+ At+yp+ ClQ++++ + + + + + g SEDCLYL
90 LREATSYPNLCQNSEWLLDQH-----MLKVHYPKFG--VSEDCLYL 130
Fbh53010FL

NVytpkntkpnSkLPVmwIhGGGfmgSghslplslYdgeslaregnVI
N+y P+ + +sklPV+Vw +GG+F +Gs+ s dg++la+ ++V
131 NIYAPAHADTGSKLPVLVWFPFGGAFKGTSA-----SIFDGSALAAAYEDVL 175
Fbh53010FL

vVsiNYRLGplGFstgddklpgsGNyGLLDQrlALKwVqdNIaaFGGDP
vV ++YRLG++GF++t d ++p GN++++DQ++AL wVq+NI FGGDP
176 VVVVQYRLGIFGFFTTWDQHAP--GNWAFKDQVAALSWVQKNIEFFGGDP 223
Fbh53010FL

nsVTifGesAGaaSVsllllsngGDNppsskgLFhRAIsqSGsalspwai
+svTifGesAGa SVs l+lS p++kgLFh+AI++SG a+ p
224 SSVTIFGESAGAISVSSlLS-----PMaKGLFHKAIMESGVAIIPYLE 267
Fbh53010FL

qsesnargrakelarilGcnetsssellddCLRksaaellleatrslife
++ + + +a + G n ++s++ll+CLR k++++ell ++++
268 AHdYEkSEdLQVVAHFcGNNASDSEALLRCLRTKPSKELLTLsq--KTKS 315
Fbh53010FL

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yvpflplflaFgPvVDgdDapeafipedPeelikeGkfadvPyliGvtkd
f+          vVDG+      f+p +P++l+ ++ f+ +P +iGv+++
Fbh53010FL  316 ---FTR-----VVDGA-----FFPNEPLDLSQKAFKAIPSIIGVNNH 350

EGgyfaam.llnasskgedelkketnpdvwllellkyllyfyasealnikdm
E+g++++m+++++ +g          ++ l++ l+ ++ +
Fbh53010FL  351 ECGFLLPMKEAPEILSG-----SNKSLALHLIQNILHIP PQ-- 386

ddladvlekyPgdvddfsvesrkpnlqdmldlFkcptrvaadlhakh
++ v ++Y+ d + s + +++ l+d+l+D++F++p ++ ++ +++
Fbh53010FL  387 --YLHLVANEYFHD-KH-SLTEIRDSLLDLLGDVFFVVP-ALITARYHRD 431

ggsPvYaYvfdhpasfgigQflakrvdpfeggavHgdeIfvFgnpllike
+g+PvY+Y+f+h+++          +++p f++a+H+dE++fvFg +lk+
Fbh53010FL  432 AGAPVYFYEFRRHPQC-----FEDTKPAFVKADHADEVRFVFGGAFLKG 475

qlyka..teeeekssktmmnywanFAktGnPnngtsnglvvWpkytsee
+   ++++teeeek+++s+++mm+ywa+FA+tGnP ng  l Wp+y+ +e
Fbh53010FL  476 DIVMFegATEEEKLLSRKMMKYWATFARTGNP-NGN--DLSLWPAYNLTE 522

qkYslllll1ttitaqklkardprkvlcnfw<-*
q  +l+ l + q+l+ +      ++fw
Fbh53010FL  523 Q--YLQDLNMSLQGLKEPR-----VDFW 545

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Fig. 2B